

FIGURE 177

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA55737

><subunit 1 of 1, 1141 aa, 1 stop

><MW: 124671, pI: 5.82, NX(S/T): 5

MAGARSRDPWGASGICYLFGSLLVELLFSRAVAFNLDVMGALRKEGEPGSLFGFSVALHRQL
QPRPQSWLLVGAPQALALPGQQANRTGGLFACPLSLEETDCYRVDIDQGADMQKESKENQWL
GVSVRSQGPGGKIVTCAHRYEARQRVDQILETRDMIGRCFVLSQDLAIRDELDDGGEWKFC
RPQGHEQFGFCQQGTAAAFSPDSHYLLFGAPGTYNWKGRTARVELCAQGSADLAHLDDGPYEA
GGEKEQDPRLI PVPANSYFGFSIDSGKGLVRAEELS FVAGAPRANHKGAVVILRKDSASRLV
PEVMLSGERLTSGFGYSLAVADLNSDGWPD LIVGAPYFFERQEELGGAVVYVLNQGHWAGI
SPLRLCGSPDSMFGISLAVLGD LNQDGF PDIAVGAPFDGDGKVFIYHGSSLGVVAKPSQVLE
GEAVGIKSFGYSLSGSLDMDGNQYPDLLVGLADTAVLFRARPILHVSHEVSIAPRSIDLEQ
PNCAGGHSVCVDLRVCFSYIAVPSSYSPTVALDYVLDADTDRLRGQVPRVTFLSRNLEEPK
HQASGTVWLKHQHDRVCGDAMFQLQENVKDKLRAIVVTLSYSLQTPRLRRQAPGQGLPPVAP
ILNAHQPS TQRAEIHFLKQCGCEDKICQSNLQLVHARFCTRVSDTEFQPLPMDVDGTTALFA
LSGQPVIGLELMVTNLPSDPAQPQADGDDAHEAQLLVMLPDSLHYSQVRLDPAEKPLCLSN
ENASHVECELGNPMKRGAQVTFYLILSTSGISIIETTELEVELLATISEQELHPVSARARVF
IELPLSIAGMAIPQQLFFSGVVRGERAMQSERDVGSKVKYEVTVSNQGQSLRTLGS AFLNIM
WPHEIANGKWL LYPMQVELEGGQGPQKGLCS PRPNILHLDVDSRDRRRRELEPPEQQEPGE
RQEPSMSWWPVSSAEKKKNITLDCARGTANCVVFSCPLYSFDRAAVLHVWGRLWNSTFLEEY
SAVKSLEIVIRANITVKSSIKNLMLRDASTVIPVMVYLDPMAVVAEGVPWWVILLAVLAGLL
VLALLVLLWKMGGFFKRAKHPEATVPQYHAVKIPREDRQQFKKEKTGTILRNNWGS PRREGP
DAHPIAADGHP ELGPDGHPGPGTA

Important features:

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 1040-1062

N-glycosylation sites.

amino acids 86-89, 746-749, 949-952, 985-988 and 1005-1008

Integrins alpha chain proteins.

amino acids 1064-1071, 384-408, 1041-1071, 317-346, 443-465, 385-407, 215-224, 634-647, 85-99, 322-346, 470-479, 442-466, 379-408 and 1031-1047

FIGURE 178

CGCGCCGGGCGCAGGGAGCTGAGTGGACGGCTCGAGACGGCGGCGCGTGCAGCAGCTCCAGA
AAGCAGCGAGTTGGCAGAGCAGGGCTGCATTTCCAGCAGGAGCTGCGAGCACAGTGCTGGCT
CACAACAAGATGCTCAAGGTGTGAGCCGTACTGTGTGTGTGTGCAGCCGCTTGGTGCAGTCA
GTCTCTCGCAGCTGCCGCGGCGGTGGCTGCAGCCGGGGGGCGGTCCGACGGCGGTAATTTTC
TGGATGATAAACAATGGCTCACCACAATCTCTCAGTATGACAAGGAAGTCGGACAGTGGAAC
AAATTCGAGACGAAGTAGAGGATGATTATTTCCGCACTTGGAGTCCAGGAAAACCTTCGA
TCAGGCTTTAGATCCAGCTAAGGATCCATGCTTAAAGATGAAATGTAGTCGCCATAAAGTAT
GCATTGCTCAAGATTCTCAGACTGCAGTCTGCATTAGTCACCGGAGGCTTACACACAGGATG
AAAGAAGCAGGAGTAGACCATAGGCAGTGGAGGGGTCCCATATTATCCACCTGCAAGCAGTG
CCCAGTGGTCTATCCCAGCCCTGTTTGTGGTTCAGATGGTCATACCTACTCTTTTCAGTGCA
AACTAGAATATCAGGCATGTGTCTTAGGAAAACAGATCTCAGTCAAATGTGAAGGACATTGC
CCATGTCCTTCAGATAAGCCCACCAGTACAAGCAGAAATGTTAAGAGAGCATGCAGTGACCT
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AGGGGTAAAGAAGCTCCTAGGACAGTATATCCCCCTGTGTGATGAAGATGGTTACTACAAGC
CAACACAATGTCATGGCAGTGTGAGCAGTGCTGGTGTGTTGACAGATATGGAAATGAAGTC
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TGCTAGTGGCGATTTTCATGAATGGACTGATGATGAGGATGATGAAGACGATATTATGAATG
ATGAAGATGAAATGAAGATGATGATGAAGATGAAGGGATGATGATGATGGTGGTGATGAC
CATGATGTATACATTTGATTGATGACAGTTGAAATCAATAAATCTACATTTCTAATATTTA
CAAAATGATAGCCTATTTAAATTTATCTTCTTCCCCAATAACAAAATGATTCTAAACCTCA
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AAATCTTCCATAAGCAAAATGACAGCTAGTGCTTGGGATCGTACATGTTAATTTTTTTGAAAG
ATAATTCTAAGTGAAATTTAAATAAATAAATTTTTTAATGACCTGGGTCTTAAGGATTTAGG
AAAAATATGCATGCTTTAATTGCATTTCCAAAGTAGCATCTTGCTAGACCTAGATGAGTCAG
GATAACAGAGAGATACCACATGACTCCAAAAAAAAAAAAAAAAA

[illegible]

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><subunit 1 of 1, 436 aa, 1 stop
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MLKVS AVLCVCAA AWCSQSLAAAAVA AAGGRSDGGNF LDDKQWLTTISQYDKEVGQWNKFR
DEVEDDYFRTWSPGK PFDQALDPAKDPCLMKKCSRHKVCIAQDSQTAVCISHRRLTHRMKEA
GVDHRQWRGPILSTCKQCPVVYPSPVCGSDGHTYSFQCKLEYQACVLGKQISVKCEGHCP
SDKPTSTSRNVKRACSDLEFREVANRLRDWFKALHESG SQNKKTLLRPERSRFDTSILPI
CKDSL GWMFNRLDTNYDLLLDQSELRSIYLDKNEQCTKAFFNSCDTYKDSLISNNEWCYCFQ
RQQDPPCQTELSNIQKRQGVKKLLGQYIPLCEDEDGYKPTQCHGSVGQCWCVD RYGN EVMGS
RINGVADCAIDFEISGDFASGDFHEWTDDEDEDEDDIMNDEDEIEDDDEDEGDDDDGGDDHDVYI

Signal peptide:

Leucine zipper pattern.

N-myristoylation sites.

Thyroglobulin type-1 repeat proteins

amino acids 353-365 and 339-352